AMENDMENTS TO THE CLAIMS

1. **(Currently Amended)** A method for identifying and/or quantifying an organism or part of an organism ~~by a detecting its nucleotide sequence among at least 4 other homologous sequences~~ **in a sample by detecting a nucleotide sequence characteristic of said organism, wherein said nucleotide sequence is homologous to at least 4 other nucleotide sequences from other organisms** comprising:

~~a. extracting original nucleotide sequences from the organism;~~

~~b.~~ amplifying or copying ~~with a unique pair of primers, at least part of original~~ **said** nucleotide sequences into target nucleotide sequences ~~to be detected~~ **using primer pairs which are capable of amplifying at least two of said homologous nucleotide sequences from other organisms**;

~~c. labelling said target nucleotide sequences;~~

~~d.~~ **contacting said amplified or copied** ~~putting into contact the labelled target~~ nucleotide sequences with single-stranded capture nucleotide sequences**, said single-stranded capture nucleotide sequences being** bound ~~by a single predetermined link~~ **in an array** to an insoluble solid support~~, preferably a non porous~~ **via a spacer which is at least 6.8 nm in length, wherein said array comprises at least 4 different bound single-stranded capture nucleotide sequences/cm^2 of** solid support~~,~~ **surface and wherein said capture nucleotide sequences comprise a nucleotide sequence of about 10 to about 60 bases which is able to specifically bind to said target nucleotide sequence without binding to said at least 4 homologous nucleotide sequences; and**

~~e. discriminating the binding of a target nucleotide sequence~~ detecting specific ~~of an organism or part of it by detecting, quantifying and/or recording a signal resulting from a~~ hybridization ~~by complementary base pairing between the~~ **of said** target nucleotide sequence **to said** ~~and its corresponding~~ capture nucleotide sequences~~,~~

~~wherein said capture nucleotide sequence being bound to the insoluble solid support at a specific location according to an array, said array having a density of at least 4 different bound single stranded capture nucleotide sequences/cm2 of solid support surface and~~

~~wherein the binding between the target nucleotide sequence and its corresponding capture nucleotide sequence forms results in said signal at the expected location, the detection of a single~~

~~signal allowing a discrimination of the target nucleotide sequence specific of an organism or part of it from homologous nucleotide sequences~~.

2. **(Currently amended)** The method according to claim 1, wherein the amplified ~~homologous original~~ nucleotide sequence is a DNA nucleotide sequence.

3. **(Canceled)**

4. **(Currently amended)** The method according to claim 1, wherein the amplified ~~homologous original~~ nucleotide sequences are mRNA first ~~retrotranscribed~~ reverse transcribed into cDNA ~~with the same primer pair~~ **and then amplified using said primer pair which is capable of amplifying at least two of said homologous mRNA in said sample**.

5-7. **(Canceled)**

8. **(Currently amended)** The method according to the claim ~~7~~ **1**, wherein said ~~spacer is a~~ **capture nucleotide sequences comprise a nucleotide sequence of between about 15 and about 40 bases which is able to specifically bind to said target nucleotide sequence without binding to said at least 4 homologous nucleotide sequences from other organisms.**

9. **(Currently amended)** The method according to claim 1, wherein the density of the capture nucleotide sequence bound to the surface at a specific location is ~~superior to~~ **more than about** 10 fmoles ~~and preferably 100 fmoles~~ per cm^2 of solid support surface.

10. **(Currently amended)** The method according to claim 1, wherein the target nucleotide sequence ~~to be detected~~ presents ~~an~~ **a** homology with other homologous nucleotide sequences higher than 30%~~, preferably higher than 60%, more preferably higher than 80%~~.

11. **(Canceled)**

12. **(Currently amended)** The method according to claim 1, ~~characterised in that~~ **wherein** other primers are present in the amplification step for the amplification of ~~other~~ **another** nucleotide ~~sequences~~ **sequence**~~, such as an antibiotic resistance determining sequence~~.

13. **(Currently amended)** The method according to claim 1, ~~characterised in that~~ wherein the insoluble solid support is selected from the group consisting of: glasses, electronic devices, silicon supports, plastic supports, compact discs, filters, filters, gel layers, **and** metallic supports ~~and a mixture thereof~~.

14. **(Currently amended)** The method according to claim 1, wherein the ~~original~~ nucleotide ~~sequences~~ **sequence** to be ~~detected~~ **identified** and/or ~~be~~ quantified ~~are~~ **is an** RNA

~~sequences~~ **sequence** submitted to a ~~retro-transcription~~ **reverse transcription** of ~~the~~ **its** 3' or 5' end by using a consensus primer ~~and possibly a stopper sequence~~.

15. **(Currently amended)** The method according to claim 1, wherein the ~~original~~ nucleotide ~~sequences~~ **sequence** to be identified and/or quantified ~~in a sample are FemA genetic sequences~~ are **from the *FemA* gene** of Staphylococci species selected from the group consisting of: *S. aureus*, *S. epidermidis*, *S. saprophyticus*, *S. hominis* ~~and/or~~ **and** *S. haemolyticus*.

16. **(Currently amended)** The method according to claim 1, wherein the solid support **also** bears capture nucleotide sequences specific of the homologous sequences specific for the binding with the homologous target nucleotide sequence together with a consensus sequence **able to bind to said target nucleotide sequence and to said at least 4 homologous nucleotide sequences** ~~for a common detection~~.

17. **(Original)** The method according to claim 1, wherein the solid support bears capture nucleotide sequences specific for the identification of two or more staphylococcus species together with a consensus sequence for a Staphylococcus genus identification.

18. **(Currently amended)** The method according to claim 1, wherein the ~~original~~ sequence to be identified and/or quantified in the sample belongs to the *MAGE* gene family.

19. **(Currently amended)** The method according to claim 1, wherein the ~~original~~ sequence to be identified and/or quantified in the sample belongs to the *HLA-A* genes family.

20. **(Currently amended)** The method according to claim 1, wherein the ~~original~~ sequence to be identified and/or quantified in the sample belongs to the dopamine receptors coupled to the protein G genes family.

21. **(Currently amended)** The method according to claim 1, wherein the ~~original~~ sequence to be identified and/or quantified in the sample belongs to the choline receptors coupled to the protein G genes family.

22. **(Currently amended)** The method according to claim 1, wherein the ~~original~~ sequence to be detected and/or quantified in the sample belongs to the histamine receptors coupled to the protein G genes family.

23. **(Currently amended)** The method according to claim 1, wherein the ~~original~~ sequence to be detected and/or quantified in the sample belongs to the cytochrome p450 forms family.

24-37. **(Withdrawn)**.

38. **(Currently amended)** The method of Claim 1, wherein said **nucleotide sequence to be identified and/or quantified originates from** ~~organism is~~ a microorganism.

39. **(Canceled)**

40. **(New)** The method according to claim 1, wherein the density of the capture nucleotide sequence bound to the surface at a specific location is more than about 100 fmoles per cm^2 of solid support surface.

41. **(New)** The method according to claim 1, wherein the target nucleotide sequence presents a homology with other homologous nucleotide sequences higher than 60%.

42. **(New)** The method according to claim 1, wherein the target nucleotide sequence presents a homology with other homologous nucleotide sequences higher than 80%.

43. **(New)** The method according to claim 1, wherein the spacer is a non-specific nucleotide sequence of at least 20 nucleotides.

44. **(New)** The method of Claim 12, wherein said other nucleotide sequence is an antibiotic resistance determining sequence.

45. **(New)** The method of Claim 1, wherein said organism is identified or quantitated by detecting a single spot signal at one specific location on said insoluble solid support.